

CD105PCT.ST25.txt  
 SEQUENCE LISTING

<110> CropDesign N.V.

<120> Plants having modified growth characteristics and method for making the same

<130> CD-105-PCT

<150> US 60/528,113  
 <151> 2003-12-09

<150> EP 03104280.7  
 <151> 2003-11-19

<160> 18

<170> PatentIn version 3.3

<210> 1  
 <211> 1428  
 <212> DNA  
 <213> Nicotiana tabacum

<220>  
 <221> misc\_feature  
 <223> seedy1 coding sequence (CDS0689)

<400> 1

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ctgaaacccc	tttcggttag	gccatcagat	tcctttgaat	ctgattttgtc	aagtaaggaa	180
aatcaaactc	ctttatttga	gaattcatct	gttaatctct	catctccgtt	accataaag	240
ccacttaacc	ctaattggggc	tctggaaaat	tcaagactca	agccgaacaa	gccaattcc	300
aaacagagtc	ttgatgagat	ggcggctaga	aagagcggaa	agggaaatga	tttccgtgat	360
gagaagaaaa	tagacgagga	aattgaagaa	attcagatgg	agattagtag	gttgagtcca	420
agattagagg	ctttgagaat	tgaaaaggct	gagaaaactg	ttgctaagac	tggtgaaaag	480
cgaggaaggg	ttgtggcagc	aaagtttatg	gagccaaaac	aaagtgttat	taagattgaa	540
gagcgtatat	caatgagtgc	aagaacaaaag	gtggagcaga	gaaggggtct	tagtttagga	600
ccatctgaga	tttttactgg	aacgcggcgg	cgagggttga	gtatggggcc	atcagatatt	660
ctagcagggg	caacaaaggc	acggcaattg	ggaaagcaag	agatgattat	tactcctatt	720
cagccaatac	aaaacaggcg	aaagtcgtgt	ttttggaagc	ttcaagagat	tgaagaagag	780
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acaaggcagg	cagttactac	aattgcatca	aagaagaatt	tgaaaaaaga	tgatggactt	900
ttgagttcag	ttcagccaaa	gaagttgttt	aaagatctcg	aaaagtctgc	tgctgctaata	960
aagaagcccc	agaggccggg	gagggttgtg	gctagtaggt	ataatcagag	tacaattcag	1020
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gataagaaac	ggtcgttatc	tgtagggaaa	acgcgtgtgt	ctcaaactga	gagcaagaat	1140
ttgggtactg	aaagtagggg	gaaaaagaga	tgggaaattc	ctagtgagat	tgtagttcat	1200
ggaaacacag	agagttagaa	atctccacta	agcattattg	tgaagcctga	tttgcttccg	1260
cgaattagga	ttgctcggtg	tgtgaatgag	actcttaggg	attctggacc	tgctaaaaga	1320
atgatagagt	tgataggcaa	gaaatcgttt	ttcagtagtg	atgaagataa	ggagccacct	1380
gtctgtcaag	ttttaagttt	tgcagaggaa	gatgctgaag	aggaataa		1428

<210> 2  
 <211> 475  
 <212> PRT  
 <213> Nicotiana tabacum

## CD105PCT.ST25.txt

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;223&gt; seedy1 protein (CDS0689)

&lt;400&gt; 2

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Met Ser Val Leu Gln Tyr Pro Glu Gly Ile Asp Pro Ala Asp Val Gln
1          5          10          15

Ile Trp Asn Asn Ala Ala Phe Asp Asn Gly Asp Ser Glu Asp Leu Ser
          20          25          30

Ser Leu Lys Arg Ser Trp Ser Pro Leu Lys Pro Leu Ser Val Arg Pro
          35          40          45

Ser Asp Ser Phe Glu Ser Asp Leu Ser Ser Lys Glu Asn Gln Thr Pro
          50          55          60

Leu Phe Glu Asn Ser Ser Val Asn Leu Ser Ser Pro Leu Pro Ile Lys
65          70          75          80

Pro Leu Asn Pro Asn Gly Ala Leu Glu Asn Ser Arg Leu Lys Pro Asn
          85          90          95

Lys Pro Asn Ser Lys Gln Ser Leu Asp Glu Met Ala Ala Arg Lys Ser
          100          105          110

Gly Lys Gly Asn Asp Phe Arg Asp Glu Lys Lys Ile Asp Glu Glu Ile
          115          120          125

Glu Glu Ile Gln Met Glu Ile Ser Arg Leu Ser Ser Arg Leu Glu Ala
          130          135          140

Leu Arg Ile Glu Lys Ala Glu Lys Thr Val Ala Lys Thr Val Glu Lys
145          150          155          160

Arg Gly Arg Val Val Ala Ala Lys Phe Met Glu Pro Lys Gln Ser Val
          165          170          175

Ile Lys Ile Glu Glu Arg Ile Ser Met Ser Ala Arg Thr Lys Val Glu
          180          185          190

Gln Arg Arg Gly Leu Ser Leu Gly Pro Ser Glu Ile Phe Thr Gly Thr
          195          200          205

Arg Arg Arg Gly Leu Ser Met Gly Pro Ser Asp Ile Leu Ala Gly Thr
          210          215          220

Thr Lys Ala Arg Gln Leu Gly Lys Gln Glu Met Ile Ile Thr Pro Ile
225          230          235          240

Gln Pro Ile Gln Asn Arg Arg Lys Ser Cys Phe Trp Lys Leu Gln Glu
          245          250          255

Ile Glu Glu Glu Gly Lys Ser Ser Ser Leu Ser Pro Lys Ser Arg Lys
          260          265          270

Thr Ala Ala Arg Thr Met Val Thr Thr Arg Gln Ala Val Thr Thr Ile
          275          280          285

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## CD105PCT.ST25.txt

Ala Ser Lys Lys Asn Leu Lys Lys Asp Asp Gly Leu Leu Ser Ser Val  
 290 295 300

Gln Pro Lys Lys Leu Phe Lys Asp Leu Glu Lys Ser Ala Ala Ala Asn  
 305 310 315 320

Lys Lys Pro Gln Arg Pro Gly Arg Val Val Ala Ser Arg Tyr Asn Gln  
 325 330 335

Ser Thr Ile Gln Ser Ser Val Val Arg Lys Arg Ser Leu Pro Glu Asn  
 340 345 350

Asp Lys Asp Glu Ser Lys Arg Asn Asp Lys Lys Arg Ser Leu Ser Val  
 355 360 365

Gly Lys Thr Arg Val Ser Gln Thr Glu Ser Lys Asn Leu Gly Thr Glu  
 370 375 380

Ser Arg Val Lys Lys Arg Trp Glu Ile Pro Ser Glu Ile Val Val His  
 385 390 395 400

Gly Asn Thr Glu Ser Glu Lys Ser Pro Leu Ser Ile Ile Val Lys Pro  
 405 410 415

Asp Leu Leu Pro Arg Ile Arg Ile Ala Arg Cys Val Asn Glu Thr Leu  
 420 425 430

Arg Asp Ser Gly Pro Ala Lys Arg Met Ile Glu Leu Ile Gly Lys Lys  
 435 440 445

Ser Phe Phe Ser Ser Asp Glu Asp Lys Glu Pro Pro Val Cys Gln Val  
 450 455 460

Leu Ser Phe Ala Glu Glu Asp Ala Glu Glu Glu  
 465 470 475

<210> 3  
 <211> 1336  
 <212> DNA  
 <213> Oryza sativa

<220>  
 <221> misc\_feature  
 <223> seedy coding sequence

<400> 3

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ggcgacaagg	agaatcaccg	ccccgaggtt	gttgatgtcg	ccgccggcta	cgacgtcgag	180
gccgagatcg	gccacatcga	ggcggagatc	ctgcgcctct	cgtccccggt	ccaccatctc	240
cgcgtctcca	agcagccgga	gcccaccgc	gacgacgctc	cgatggggga	gatggtcgcg	300
aaggtgaggc	cccggccgag	gggcctcagc	ctcggggccc	tggatgtgat	ctccatcgtc	360
aatcgtgaga	agcatccgct	gcgcaccaag	cagcctccgg	cgacgcgggg	cagggggctc	420
agcctcgggc	ccatggagat	cgccgcggcg	aaccctaggg	tgcccgcggc	ggcgcagcat	480
cagcaacagc	aacgcgctgg	cacggcgcg	atcctgaagc	caatcaagga	gcctccggtg	540
cagcgtcgca	ggggcgctcag	cctcggggcg	ttggagatcc	accacggcgt	cggcagcaag	600
gcaccagcgg	cggcgcgagc	caagccgttc	accaccaagc	tcaacgccat	tcgagaagaa	660
acccgaccct	ccaagcaatt	cgccgtcccc	gccaagccat	ggccgtcgag	caatacaagg	720
cagacactgg	actcgaggca	aggaacagca	gcaagtcgag	cgaaggcgag	gagcccgcgc	780

## CD105PCT.ST25.txt

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cccaggccca ggaggcaatc caatggcaag gctactgaca caaggggagg caacaaggtg      840
gtggatgagc tcaagcccaa aggtgcgtcg tcaagtcaga gcggcagcgc cgccgccgcc      900
gccactgcca agaggatggc ggggagctcc aagatgaggg tcatcccgag ccgctacagc      960
ctcactcctg gcgcttcctt tggaagcagt ggagcacagg agaggcgacg caagcagtct    1020
ctcccaggat catcagggga tgcgaaccag aatgaggaaa tcagagcgaa ggtcatcgag    1080
ccttccaatg atccactctc tcctcaaacg atctccaagg ttgctgaaat gctcccaaag    1140
atcaggacca tgccgcctcc tgacgagagc cctcgcgatt ccggatgcgc caagcggggt    1200
gccgaattgg tcgggaagcg ctcgttcttc acggtgcgag ccgaggacgg gcgggcgctc    1260
gacgtcgaag cacccgaggc ggtcgcagaa gcttgagatg aaccaccatg gtttgatccg    1320
ttccttccat cagctc                                     1336

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<210> 4  
 <211> 431  
 <212> PRT  
 <213> Oryza sativa

<220>  
 <221> MISC\_FEATURE  
 <223> seedy1 protein

<400> 4

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Met Glu Glu Asp Pro Leu Ile Pro Leu Val His Val Trp Asn Asn Ala
1          5          10          15

Ala Phe Asp Asp Ser Ser Cys Ser Arg Ser Ala Trp Leu Pro Gln Ser
20          25          30

Pro Ala Val Ala Ala Val Arg Lys Gly Asp Lys Glu Asn His Arg Pro
35          40          45

Glu Val Val Asp Val Ala Ala Gly Tyr Asp Val Glu Ala Glu Ile Gly
50          55          60

His Ile Glu Ala Glu Ile Leu Arg Leu Ser Ser Arg Leu His His Leu
65          70          75          80

Arg Val Ser Lys Gln Pro Glu Pro Asn Arg Asp Asp Ala Pro Met Gly
85          90          95

Glu Met Val Ala Lys Val Arg Pro Arg Pro Arg Gly Leu Ser Leu Gly
100         105         110

Pro Leu Asp Val Ile Ser Ile Val Asn Arg Glu Lys His Pro Leu Arg
115         120         125

Thr Lys Gln Pro Pro Ala Thr Arg Gly Arg Gly Leu Ser Leu Gly Pro
130         135         140

Met Glu Ile Ala Ala Ala Asn Pro Arg Val Pro Ala Ala Ala Gln His
145         150         155         160

Gln Gln Gln Gln Arg Ala Gly Thr Ala Arg Ile Leu Lys Pro Ile Lys
165         170         175

Glu Pro Pro Val Gln Arg Arg Arg Gly Val Ser Leu Gly Pro Leu Glu
180         185         190

Ile His His Gly Val Gly Ser Lys Ala Pro Ala Ala Ala Arg Ala Lys
195         200         205

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## CD105PCT.ST25.txt

Pro Phe Thr Thr Lys Leu Asn Ala Ile Arg Glu Glu Thr Arg Pro Ser  
 210 215 220  
 Lys Gln Phe Ala Val Pro Ala Lys Pro Trp Pro Ser Ser Asn Thr Arg  
 225 230 235 240  
 Gln Thr Leu Asp Ser Arg Gln Gly Thr Ala Ala Ser Arg Ala Lys Ala  
 245 250 255  
 Arg Ser Pro Ser Pro Arg Pro Arg Arg Gln Ser Asn Gly Lys Ala Thr  
 260 265 270  
 Asp Thr Arg Gly Gly Asn Lys Val Val Asp Glu Leu Lys Pro Lys Gly  
 275 280 285  
 Ala Ser Ser Ser Gln Ser Gly Ser Ala Ala Ala Ala Thr Ala Lys  
 290 295 300  
 Arg Met Ala Gly Ser Ser Lys Met Arg Val Ile Pro Ser Arg Tyr Ser  
 305 310 315 320  
 Leu Thr Pro Gly Ala Ser Leu Gly Ser Ser Gly Ala Gln Glu Arg Arg  
 325 330 335  
 Arg Lys Gln Ser Leu Pro Gly Ser Ser Gly Asp Ala Asn Gln Asn Glu  
 340 345 350  
 Glu Ile Arg Ala Lys Val Ile Glu Pro Ser Asn Asp Pro Leu Ser Pro  
 355 360 365  
 Gln Thr Ile Ser Lys Val Ala Glu Met Leu Pro Lys Ile Arg Thr Met  
 370 375 380  
 Pro Pro Pro Asp Glu Ser Pro Arg Asp Ser Gly Cys Ala Lys Arg Val  
 385 390 395 400  
 Ala Glu Leu Val Gly Lys Arg Ser Phe Phe Thr Ala Ala Ala Glu Asp  
 405 410 415  
 Gly Arg Ala Leu Asp Val Glu Ala Pro Glu Ala Val Ala Glu Ala  
 420 425 430

<210> 5  
 <211> 1860  
 <212> DNA  
 <213> Medicago trunculata  
 <220>  
 <221> misc\_feature  
 <223> seedyl coding sequence

<400> 5  
 aaaaacgtta aggactaaaa atataataaa atttaagtag ggattcataa tggaagcacc 60  
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 aatcacatcg gagcgtgtat gagtagccgt ttcacatcca acggccagta agagcgtaac 180  
 tttatttctt cctctttcaa tctccaacgg tcacataatc tcttccaaat acaaataatt 240  
 ccctctttca acctcactct tcatttcttc aacccaaacc caaaaaacta atcagattct 300  
 tcttaaactc tgaaaccttt ctcccaaaag cacttaaata aaaaagcact taaccatgaa 360

## CD105PCT.ST25.txt

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taacacaaac aacaacaaca ttctttcttca ttccacacag gttcaagtgt ggaacaacgc 420
agcattcgat ggtgaagatt tcgccatgaa ttcatcttct gattccatca aagagaatct 480
aaacccatcc gcattcaaca ttgttccttc ttcaaacaaa agaactattg atgatgaaat 540
tgcggaattt gaaagtgaag ttaagcgatt aacttcgaag ctggaattgc ttcgtgttga 600
aaaagctgaa agaaaaatcg cttctgaaaa gcgtgttagt ggaatttgta ctggaagaat 660
agtagcagcg aagtttatgg aaccgaagaa aaacgttaca ccgaaacgaa acggtgtcgt 720
tttcaaggag gagacaccga aacgaaacgg tgctgtttcg gatacgccga aatctagggg 780
taattggaga agagggatga gtttaggtcc gatggagatt gccgggaaag tgatggcacc 840
gccggcgatg acgattactc cggcgacggt gaatcggagg aagtcttggt tctggaaacc 900
gcaggaaagt tgtgaagtaa tgccgtcggg gattactccg gcgacggtga ataggaggaa 960
atcttgtttt ttgaaacctc aagaaaagttg tgaagaaaaa cgaagaaaaa cgatttgcaa 1020
accgaatttg aatttgaatt caaattcagt taattctgcg gttggatcga ttaagcgtgt 1080
gaagaagaaa gatgaagaaa ttgctcaggt tcaaccgaag aagctgtttg aaggtgaaaa 1140
atcagtgaag aaatcggtga aacaaggtag aattgttgca agccggtata attccggtgg 1200
tggtggtggt gatgagagga aaagatcgtt ttcggagaat aataagggtt tagggagtga 1260
aatcagggct aagaagagat gggagatacc aattgaagaa gtggatgtga gtggttttgt 1320
tatgttaccg aagattttcga caatgaggtt tgttgatgag agtcctagag attctggtgc 1380
tgttaaaaga gttgctgaat tgaatgaaa aagatcttac ttttgtgatg aagatgagga 1440
ggagagagtg atggtggagg aagaaggtag tctgtttgt caggttttga attttgctga 1500
agatgatgat gatgatgatg attatggtga acaagggtaa ttgtggaaat tgggaattgat 1560
ttgtttttgt ggggttgtgt ggaactggct atgttctgct tgattctttt gcattttggt 1620
gtgaaactaa agatgaggtg aaaagtttat gcttgttaaa ttggattggt ttatatgttt 1680
tgaaataata acaacaagca tgtgtcttgc ttaataattg tatattgttt tgtttgtttt 1740
ataatgatat ggatttaatt tgtatacaca atataatata gtatgcattg agagagtttt 1800
tcgttcagta ttcattctga ttttagtggt tatctcattc tagaagattg tattttgttg 1860

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<210> 6  
<211> 394  
<212> PRT  
<213> Medicago trunculata

<220>  
<221> MISC FEATURE  
<223> seedy1 protein

<400> 6  
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Gln Val Trp Asn Asn Ala Ala Phe Asp Gly Glu Asp Phe Ala Met Asn  
20 25 30  
Ser Ser Ser Asp Ser Ile Lys Glu Asn Leu Asn Pro Ser Ala Phe Asn  
35 40 45  
Ile Val Pro Ser Ser Asn Lys Arg Thr Ile Asp Asp Glu Ile Ala Glu  
50 55 60  
Ile Glu Ser Glu Ile Lys Arg Leu Thr Ser Lys Leu Glu Leu Leu Arg  
65 70 75 80  
Val Glu Lys Ala Glu Arg Lys Ile Ala Ser Glu Lys Arg Val Ser Gly  
85 90 95  
Ile Gly Thr Gly Arg Ile Val Ala Ala Lys Phe Met Glu Pro Lys Lys  
100 105 110  
Asn Val Thr Pro Lys Arg Asn Gly Val Val Phe Lys Glu Glu Thr Pro  
115 120 125

## CD105PCT.ST25.txt

Lys Arg Asn Gly Val Val Ser Asp Thr Pro Lys Ser Arg Val Asn Trp  
 130 135 140  
 Arg Arg Gly Met Ser Leu Gly Pro Met Glu Ile Ala Gly Lys Val Met  
 145 150 155 160  
 Ala Pro Pro Ala Met Thr Ile Thr Pro Ala Thr Val Asn Arg Arg Lys  
 165 170 175  
 Ser Cys Phe Trp Lys Pro Gln Glu Ser Cys Glu Val Met Pro Ser Gly  
 180 185 190  
 Ile Thr Pro Ala Thr Val Asn Arg Arg Lys Ser Cys Phe Leu Lys Pro  
 195 200 205  
 Gln Glu Ser Cys Glu Glu Asn Arg Arg Lys Thr Ile Cys Lys Pro Asn  
 210 215 220  
 Leu Asn Leu Asn Ser Asn Ser Val Asn Ser Ala Val Gly Ser Ile Lys  
 225 230 235 240  
 Arg Val Lys Lys Lys Asp Glu Glu Ile Ala Gln Val Gln Pro Lys Lys  
 245 250 255  
 Leu Phe Glu Gly Glu Lys Ser Val Lys Lys Ser Leu Lys Gln Gly Arg  
 260 265 270  
 Ile Val Ala Ser Arg Tyr Asn Ser Gly Gly Gly Gly Gly Asp Ala Arg  
 275 280 285  
 Lys Arg Ser Phe Ser Glu Asn Asn Lys Gly Leu Gly Ser Glu Ile Arg  
 290 295 300  
 Ala Lys Lys Arg Trp Glu Ile Pro Ile Glu Glu Val Asp Val Ser Gly  
 305 310 315 320  
 Phe Val Met Leu Pro Lys Ile Ser Thr Met Arg Phe Val Asp Glu Ser  
 325 330 335  
 Pro Arg Asp Ser Gly Ala Val Lys Arg Val Ala Glu Leu Asn Gly Lys  
 340 345 350  
 Arg Ser Tyr Phe Cys Asp Glu Asp Glu Glu Glu Arg Val Met Val Glu  
 355 360 365  
 Glu Glu Gly Gly Ser Val Cys Gln Val Leu Asn Phe Ala Glu Asp Asp  
 370 375 380  
 Asp Asp Asp Asp Asp Tyr Gly Glu Gln Gly  
 385 390

<210> 7  
 <211> 674  
 <212> DNA  
 <213> Saccharum sp.

<220>  
 <221> misc\_feature

## CD105PCT.ST25.txt

<223> seedyl coding sequence (partial 5' end)

<220>

<221> misc\_feature

<222> (362)..(362)

<223> n can be a, c, g or t

<220>

<221> misc\_feature

<222> (372)..(372)

<223> n can be a, c, g or t

<220>

<221> misc\_feature

<222> (674)..(674)

<223> n can be a, c, g or t

<400> 7

cgcaccgcga	gttttcgaaaa	accaaactat	cgcgcctcag	atcacgcgag	gacgcgaggg	60
gaagcaggaa	tccctccgct	cccagccgcc	tcctccgctc	acccatcgat	cgatcgccg	120
tccggtccag	ggggctctcc	ggcggcgggtg	gcgatggagg	aggacccgct	catcccgtg	180
gtgcacgtct	ggaacaacgc	cgccttcgac	cacgcctcct	cctccgcgtg	gcacgcccac	240
tcccctgtgc	ccgcgagcgc	acgtcgcgag	gcggaggggg	acaaggagaa	ccaccgcccc	300
gaccccgacc	ccgacgtcga	ggcggagatc	ggccacatcg	aggcggagat	cctgcgcctg	360
tnctcccgcc	tncaaacct	tcgcacctcc	aagcagtcgg	agccgtccaa	gcgcggagag	420
gtcgcgccc	cgcccgcggc	gaaggcgaaa	gcggcgggcg	cggcgcggct	gcggacgcgg	480
gggtccagcc	tgggcccgt	cgacgtcgcc	gctgcggta	acccaaccc	gctcaccacc	540
gacaaccagc	agcagcagcc	gcgtgccgcg	cagggtctga	agccgatcaa	gcaggccacg	600
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ggteccctcc	cccn					674

<210> 8

<211> 166

<212> PRT

<213> Saccharum sp.

<220>

<221> MISC\_FEATURE

<223> seedyl protein

<220>

<221> MISC\_FEATURE

<223> seedyl protein (partial N term)

<220>

<221> MISC\_FEATURE

<222> (70)..(70)

<223> Xaa can be any amino acid

<400> 8

Met	Glu	Glu	Asp	Pro	Leu	Ile	Pro	Leu	Val	His	Val	Trp	Asn	Asn	Ala
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Ala	Phe	Asp	His	Ala	Ser	Ser	Ser	Ala	Trp	His	Ala	His	Ser	Pro	Val
			20					25					30		
Pro	Ala	Ser	Ala	Arg	Arg	Glu	Ala	Glu	Gly	Asp	Lys	Glu	Asn	His	Arg
			35				40					45			



## CD105PCT.ST25.txt

Pro Asp Pro Asp Pro Asp Val Glu Ala Glu Ile Gly His Ile Glu Ala  
 50 55 60

Glu Ile Leu Arg Leu Xaa Ser Arg Leu His His Leu Arg Thr Ser Lys  
 65 70 75 80

Gln Ser Glu Pro Ser Lys Arg Gly Glu Val Ala Pro Ala Pro Ala Ala  
 85 90 95

Lys Ala Lys Ala Ala Ala Ala Ala Arg Leu Arg Thr Arg Gly Leu Ser  
 100 105 110

Leu Gly Pro Leu Asp Val Ala Ala Ala Gly Asn Pro Asn Pro Leu Thr  
 115 120 125

Thr Asp Asn Gln Gln Gln Gln Pro Arg Ala Ala Gln Gly Leu Lys Pro  
 130 135 140

Ile Lys Gln Ala Thr Ala Ala Ala Gly Lys Gly Val Arg Leu Gly Pro  
 145 150 155 160

Leu Arg His Gly Arg Arg  
 165

<210> 9  
 <211> 876  
 <212> DNA  
 <213> Zea mays

<220>  
 <221> misc\_feature  
 <223> seedy1 coding sequence (partial 3' end)

<220>  
 <221> misc\_feature  
 <222> (869)..(869)  
 <223> n = a, c, g or t

<400> 9

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caagcagagc	caaggcgagg	agcgggagca	taagccccag	caggttcagg	aggcagtcca	180
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ggagcgaagc	ggtcaatcac	accagcaatg	tagccacgac	gaagaggccg	gcggggagct	300
ccaaggtcag	ggttgtcccg	agccgtaca	gcacccacc	tggctcctcc	ctagcagctg	360
tgacacaagg	caaccgatgc	aagcagtctc	tcccaggatc	ggctactgag	accagagtaa	420
atctcactga	gccgccgaac	gacgagttgt	ctcctgaaga	acttgccaag	gttgacagagc	480
tgctcccaag	gattaggacc	atgccgcctt	ctgatgagag	cccgcgtgac	tcgggatgtg	540
ccaagcgtgt	tgctgatttg	gtcgggaagc	gaccccttctt	cactgctgca	ggggacgatg	600
gcaatctcgt	tacgccctac	caggcacggg	tggttgaaact	tgaatcacc	gaggcagcag	660
cagaagaagc	agaagccttga	gaagtttgtc	tttgatcaat	tccgaagtgg	cttgcatctg	720
ggcgtggcct	ctttttgacg	tgtgtgctac	tacatagtct	actgttacat	tcatatcata	780
tcacatttcc	tattttttcc	cccttgagac	attgcttagt	acttttgtgt	tgcttgtga	840
aaagagagtg	gaaggttcat	ctgctgatnc	cttggt			876

<210> 10  
 <211> 224  
 <212> PRT  
 <213> Zea mays

## CD105PCT.ST25.txt

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;223&gt; seedy1 protein (partial C term)

&lt;400&gt; 10

Thr Arg Pro Ala Val Arg Glu Glu Glu Gly Gln Arg Ser Lys Glu His  
 1 5 10 15

Ala Val Pro Ala Arg Pro Trp Pro Ser Ser Asn Ala Arg His Pro Leu  
 20 25 30

Asp Ala Arg Gln Gly Thr Ala Ala Ser Arg Ala Lys Ala Arg Ser Gly  
 35 40 45

Ser Ile Ser Pro Ser Arg Phe Arg Arg Gln Ser Thr Ser Lys Ala Ala  
 50 55 60

Glu Thr Arg Ala Gly Asn Ala Lys Pro Thr Glu Ala Thr Arg Gly Gly  
 65 70 75 80

Ser Glu Ala Val Asn His Thr Ser Asn Val Ala Thr Thr Lys Arg Pro  
 85 90 95

Ala Gly Ser Ser Lys Val Arg Val Val Pro Ser Arg Tyr Ser Ile Pro  
 100 105 110

Pro Gly Ser Ser Leu Ala Ala Val Thr Gln Gly Asn Arg Cys Lys Gln  
 115 120 125

Ser Leu Pro Gly Ser Ala Thr Glu Thr Arg Val Asn Leu Thr Glu Pro  
 130 135 140

Pro Asn Asp Glu Leu Ser Pro Glu Glu Leu Ala Lys Val Ala Glu Leu  
 145 150 155 160

Leu Pro Arg Ile Arg Thr Met Pro Pro Ser Asp Glu Ser Pro Arg Asp  
 165 170 175

Ser Gly Cys Ala Lys Arg Val Ala Asp Leu Val Gly Lys Arg Ser Phe  
 180 185 190

Phe Thr Ala Ala Gly Asp Asp Gly Asn Leu Val Thr Pro Tyr Gln Ala  
 195 200 205

Arg Val Val Glu Leu Glu Ser Pro Glu Ala Ala Ala Glu Glu Ala Glu  
 210 215 220

&lt;210&gt; 11

&lt;211&gt; 1257

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; seedy1 coding sequence

&lt;400&gt; 11

atgacatcaa ttgaggcaac agaaacgctt aacgctcctc caaagcttca gatctggaac

60

## CD105PCT.ST25.txt

```

aacgctgcct tcgacgatgg agattctcaa atcacttccg ccatcgaagc ttctttcttgg 120
tctcacctca acgaatcatt cgattccgat tgtagcaagg agaatcagtt tccgatttcg 180
gtttcctctt cgctccaatc ctcagtcctg atcacccaag ctccgtcagc aaaatccaag 240
accgtgaaga ccaaattccgc cgcagatcgg agtaaaaagc gagatatcga tgcagagatc 300
gaagaagtag agaaggagat cggacgatta tcgacgaaat tggagtcgct ccgattagag 360
aaggcggagc aaaccgcaag aagcattgct atacgtggaa gaatcgttcc ggcgaagttc 420
atggaatcat ctcagaaaca agtgaaattc gacgattcgt gttttacagg atcgaaatca 480
agagccactc gtagaggcgt tagtcttggg ccagcggaga tattcaattc cgcgaagaaa 540
tctgaaactg tgactcctct tcaatcagct cagaatcgac gcaagtcttg tttctttaag 600
cttcctggaa tcgaagaagg tcaagtgcgc acacgaggtg aaggaagaac gagtttgagt 660
ctgagtcgga gatctcgcaa agcgaaaatg acggcagctc agaagcaagc agctacgacg 720
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gcttctgatg aaagtaacaa gagtgaaggg agagtgaaga agagatggga gattccaagt 1020
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&lt;210&gt; 12

&lt;211&gt; 402

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;223&gt; seedy1 protein

&lt;400&gt; 12

```

Met Thr Ser Ile Glu Ala Thr Glu Thr Leu Asn Ala Pro Pro Lys Leu
1           5           10           15

```

```

Gln Ile Trp Asn Asn Ala Ala Phe Asp Asp Gly Asp Ser Gln Ile Thr
20           25           30

```

```

Ser Ala Ile Glu Ala Ser Ser Trp Ser His Leu Asn Glu Ser Phe Asp
35           40           45

```

```

Ser Asp Cys Ser Lys Glu Asn Gln Phe Pro Ile Ser Val Ser Ser Ser
50           55           60

```

```

Leu Gln Ser Ser Val Ser Ile Thr Glu Ala Pro Ser Ala Lys Ser Lys
65           70           75           80

```

```

Thr Val Lys Thr Lys Ser Ala Ala Asp Arg Ser Lys Lys Arg Asp Ile
85           90           95

```

```

Asp Ala Glu Ile Glu Glu Val Glu Lys Glu Ile Gly Arg Leu Ser Thr
100          105          110

```

```

Lys Leu Glu Ser Leu Arg Leu Glu Lys Ala Glu Gln Thr Ala Arg Ser
115          120          125

```

```

Ile Ala Ile Arg Gly Arg Ile Val Pro Ala Lys Phe Met Glu Ser Ser
130          135          140

```

```

Gln Lys Gln Val Lys Phe Asp Asp Ser Cys Phe Thr Gly Ser Lys Ser

```

## CD105PCT.ST25.txt

145                      150                      155                      160  
 Arg Ala Thr Arg Arg Gly Val Ser Leu Gly Pro Ala Glu Ile Phe Asn  
                                  165                      170                      175  
 Ser Ala Lys Lys Ser Glu Thr Val Thr Pro Leu Gln Ser Ala Gln Asn  
                                  180                      185                      190  
 Arg Arg Lys Ser Cys Phe Phe Lys Leu Pro Gly Ile Glu Glu Gly Gln  
                                  195                      200                      205  
 Val Thr Thr Arg Gly Lys Gly Arg Thr Ser Leu Ser Leu Ser Pro Arg  
                                  210                      215                      220  
 Ser Arg Lys Ala Lys Met Thr Ala Ala Gln Lys Gln Ala Ala Thr Thr  
                                  225                      230                      235                      240  
 Val Gly Ser Lys Arg Ala Val Lys Lys Glu Glu Gly Val Leu Leu Thr  
                                  245                      250                      255  
 Ile Gln Pro Lys Arg Leu Phe Lys Glu Asp Glu Lys Asn Val Ser Leu  
                                  260                      265                      270  
 Arg Lys Pro Leu Lys Pro Gly Arg Val Val Ala Ser Arg Tyr Ser Gln  
                                  275                      280                      285  
 Met Gly Lys Thr Gln Thr Gly Glu Lys Asp Val Arg Lys Arg Ser Leu  
                                  290                      295                      300  
 Pro Glu Asp Glu Glu Lys Glu Asn His Lys Arg Ser Glu Lys Arg Arg  
                                  305                      310                      315                      320  
 Ala Ser Asp Glu Ser Asn Lys Ser Glu Gly Arg Val Lys Lys Arg Trp  
                                  325                      330                      335  
 Glu Ile Pro Ser Glu Val Asp Leu Tyr Ser Ser Gly Glu Asn Gly Asp  
                                  340                      345                      350  
 Glu Ser Pro Ile Val Lys Glu Leu Pro Lys Ile Arg Thr Leu Arg Arg  
                                  355                      360                      365  
 Val Gly Gly Ser Pro Arg Asp Ser Gly Ala Ala Lys Arg Val Ala Glu  
                                  370                      375                      380  
 Leu Gln Ala Lys Asp Arg Asn Phe Thr Phe Cys Gln Leu Leu Lys Phe  
                                  385                      390                      395                      400  
 Glu Glu

<210> 13  
 <211> 3074  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Sequence of the [PRO0090 - CDS0689 - terminator] expression cassette

## CD105PCT.ST25.txt

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<400> 13
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ttattttaca aaaatataaa atagatcagt ccctcaccac aagtagagca agttggtgag 120
ttattgtaaa gttctacaaa gctaatttaa aagttattgc attaacttat ttcattattac 180
aaacaagagt gtcaatggaa caatgaaaac catatgacat actataattt tgtttttatt 240
attgaaatta tataattcaa agagaataaa tccacatagc cgtaaaagttc tacatgtggt 300
gcattaccaa aatatatata gcttacaaaa catgacaagc ttagtttgaa aaattgcaat 360
ccttatcaca ttgacacata aagttagtga tgagtcataa tattattttc tttgctaccc 420
atcatgtata tatgatagcc acaaagttac tttgatgatg atatcaaaga acatttttag 480
gtgcacccctc cagaatatcc aaataatatg actcacttag atcataatag agcatcaagt 540
aaaactaaca ctctaaagca accgatggga aagcatctat aaatagacaa gcacaatgaa 600
aatcctcatc atccttcacc acaattcaaa tattatagtt gaagcatagt agtaatttaa 660
atcaactagg gatatacaaa gtttgtaaaa aaaagcaggc tggtagcggg ccggaattcc 720
cgggatatcg tcgacccacg cgtccgctga cgcgtgggtt ccactacatc aagacatcta 780
ctacactcat cttttttgca cttattgggt gtaaatTTTT gaaacccagt tgagaaaaat 840
gagtgtgtta caatacccag aagggattga ccagcagat gttagatat ggaacaatgc 900
agcatttgat aatggagatt ctgaagattt gtcttcgctg aaacgttctt ggtctcctct 960
gaaacccctt tcggttaggc catcagattc ctttgaattc gatttgtcaa gtaaggaaaa 1020
tcaaactcct ttatttgaga attcatctgt taatctctca tctccgttac ccataaagcc 1080
acttaaccct aatggggctc tggaaaattc aagactcaag ccgaacaagc ccaattccaa 1140
acagagtctt gatgagatgg cggctagaaa gagcggaaaag ggaaatgatt tccgtgatga 1200
gaagaaaaata gacgaggaaa ttgaagaaat tcagatggag attagtaggt tgagtccaag 1260
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gcgtatatca atgagtgcac gaacaaaggc ggagcagaga aggggtctta gtttaggacc 1440
atctgagatt tttactggaa cgcggcgcg aggggtgagt atggggccat cagatattct 1500
agcagggaca acaaggcac ggcaattggg aaagcaagag atgattatta ctctatttca 1560
gccaatacaa aacaggcgaa agtcgtgttt ttggaagctt caagagattg aagaagaggg 1620
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agctgctaac tcttttcatg ctctttcaat tttcaatcct gccttttaat ttttgttcat 2340
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gttagttttt agcttaaaat agatgcgga gcggccgctc tagagtatcc ctcgaggggc 2520
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acctgaatga acaattgaaa tgaaaagaaa aaaagtactc catctgttcc aaattaaaat 2760
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atttgttatc atccgggagg tcttctaggg ataacagggt aattatatcc ctctagacaa 2880
cacacaacaa ataagagaaa aaacaaataa tattaatttg agaatgaaca aaaggaccat 2940
atcattcatt aactcttctc catccatttc catttcacag ttcgatagcg aaaaccgaat 3000
aaaaaacaca gtaaatfaca agcacaacaa atggtacaag aaaaacagtt ttcccaatgc 3060
cataatactc gaac 3074

<210> 14
<211> 668
<212> DNA
<213> Oryza sativa

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## CD105PCT.ST25.txt

<220>  
 <221> misc\_feature  
 <223> prolamin RP6 promoter sequence

<400> 14  
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 attattttac aaaaatataa aatagatcag tccctcacca caagtagagc aagttggtga 120  
 gttattgtaa agttctacaa agctaattta aaagttattg cattaactta ttcatatta 180  
 caaacaagag tgtcaatgga acaatgaaaa ccatatgaca tactataatt ttgtttttat 240  
 tattgaaatt atataattca aagagaataa atccacatag ccgtaaagtt ctacatgtgg 300  
 tgcattacca aaatatatat agcttacaaa acatgacaag cttagtttga aaaattgcaa 360  
 tccttatcac attgacacat aaagtgagtg atgagtcata atattatttt tcttgctacc 420  
 catcatgtat atatgatagc cacaagttta ctttgatgat gatatcaaag aacattttta 480  
 ggtgcaccta acagaatatc caaataatat gactcactta gatcataata gagcatcaag 540  
 taaaactaac actctaaagc aaccgatggg aaagcatcta taaatagaca agcacaatga 600  
 aaatcctcat catccttcac cacaattcaa atattatagt tgaagcatag tagtagaatc 660  
 caacaaca 668

<210> 15  
 <211> 7  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Motif 1 CORE SEQUENCE

<220>  
 <221> MISC\_FEATURE  
 <222> (2)..(2)  
 <223> Xaa can be any amino acid

<220>  
 <221> MISC\_FEATURE  
 <222> (5)..(6)  
 <223> Xaa can be any amino acid

<400> 15  
 Trp Xaa Asn Ala Xaa Xaa Asp  
 1 5

<210> 16  
 <211> 6  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Motif 2 CORE SEQUENCE

<220>  
 <221> MISC\_FEATURE  
 <222> (4)..(5)  
 <223> Xaa can be any amino acid

<400> 16  
 Lys Glu Asn Xaa Xaa Pro  
 1 5

<210> 17  
 <211> 15

## CD105PCT.ST25.txt

```

<212> PRT
<213> Artificial sequence

<220>
<223> Motif 3 (coiled coil) CORE SEQUENCE

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> Xaa can be a stretch of 1 to 6 amino acids

<220>
<221> MISC_FEATURE
<222> (4)..(5)
<223> Xaa can be any amino acid

<220>
<221> MISC_FEATURE
<222> (8)..(10)
<223> Xaa can be any amino acid

<220>
<221> MISC_FEATURE
<222> (12)..(13)
<223> Xaa can be any amino acid

<400> 17
Glu Xaa Glu Xaa Xaa Arg Leu Xaa Xaa Xaa Leu Xaa Xaa Leu Arg
1          5          10          15

<210> 18
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Motif 4 CORE SEQUENCE

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa can be any amino acid

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa can be a stretch of 1 to 10 amino acids

<220>
<221> MISC_FEATURE
<222> (10)..(11)
<223> Xaa can be any amino acid

<220>
<221> MISC_FEATURE
<222> (14)..(14)
<223> Xaa can be a stretch of 1 to 6 amino acids

<400> 18

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## CD105PCT.ST25.txt

Leu	Pro	Xaa	Ile	Xaa	Arg	Asp	Ser	Gly	Xaa	Xaa	Lys	Arg	Xaa	Lys
1				5					10					15